

09916790-072704

ACGCAACTTCGGGCCCAGGGGTCCGCCCCAAGGGGTCCGAAGAGCCTTGAACCGGCCCCGGCTCCTTGACCTTGCTTGT SEQ ID NO:1
 GGGCCGAAGGACTGCCCCCTGGGCTGGGTCCGGGTGTGCCCCCTTCTCACTTGAAGACA.GCAGGCCCTGACTCTCCG
 CACACTTGGCCCCGCCAGCGACGTCACCCAAGCACCTACGAACTAGTCCCGGAGCTGGGCAAAGGCACCTACGGGAAG

GTGATCTGGTGGTCTACAAGGGCACAGGCACAAAA	M A L K F V N K S K	10
ATG GCA CTG AAG TTT GTG AAC AAG AGC AAA		SEQ ID NO:2
↑SEQ ID NO:3→		30
T K L K N F L R E V S I T N S L S S S P		30
ACC AAG CTG AAG AAC TTC CTA CGG GAG GTG AGC ATC ACC AAC AGC CTC TCC TCC AGC CCC		90
F I I K V F D V V F E T E D C Y V F A Q		50
TTC ATC ATC AAG GTC TTT GAC GTG GTC TTT GAG ACA GAG GAC TGC TAC GTC TTT GCC CAG		150
E Y A P A G D L F D I I P P Q V G L P E		70
GAG TAC GCA CCT GCT GGG GAC CTG TTT GAC ATC ATC CCT CCC CAG GTG GGG CTC CCT GAG		210
D T V K R C V Q Q L G L A L D F M H G R		90
GAC ACG GTG AAG CGC TGT GTG CAG CAG CTG GGC CTG GCG CTG GAC TTC ATG CAC GGG CGG		270
Q L V H R D I K P E N V L L F D R E C R		110
CAG CTG GTG CAC CGC GAC ATC AAG CCC GAG AAC GTG CTG CTG TTC GAC CGC GAG TGC CGC		330
R V K L A D F G M T R R V G C R V K R V		130
CGC GTA AAG CTG GCC GAC TTC GGC ATG ACG CGC CGC GTG GGC TGC CGC GTC AAG CGC GTG		390
S G T I P Y T A P E V C Q A G R A D G L		150
AGC GGC ACC ATC CCT TAC ACG GCG CCT GAG GTG TGC CAG GCG GGC CGC GCC GAC GGG CTG		450
A V D T G V D V W A F G V L I F C V L T		170
CGC GTG GAC ACG GGC GTG GAC GTG TGG GCC TTC GGC GTG CTC ATC TTC TGC GTG CTC ACC		510
G N F P W E A A S G A D A F F E E F V R		190
GGC AAC TTC CCG TGG GAG GCG GCG TCG GGC GCC GAC GCC TTC TTC GAG GAG TTC GTG CGC		570
W Q R G R L P G L P S Q W R R F T E P A		210
TGG CAG CGG GGC CGC CTG CCG GGG CTG CCT TCG CAG TGG CGC CGC TTC ACC GAG CCC GCG		630
L R M F Q R L L A L E P E R R G P A K E		230
CTG CGC ATG TTC CAG CGC TTA CTG GCC CTG GAG CCC GAG CGC CGC GGC CCA GCC AAG GAG		690
V F R F L K H E L T S E L R R R P S H R		250
GTG TTC CGC TTC CTC AAG CAC GAG CTC ACG TCC GAG CTG CGC CGC CGG CCC TCG CAC CGC		750
A R K P P G D R P P A A G P L R L E A P		270
GCG CGC AAG CCC CCC GGG GAC CGC CCG CCC GCC GCC GGG CCA CTG CGC CTC GAG GCG CCT		810
G P L K R T V L T E S G S G S R P A P P		290
GGG CCG CTC AAG CGG ACG GTG CTG ACC GAG AGC GGC AGC GGC TCC CGG CCC GCG CCC CCC		870
A V G S V P L P V P V P V P V P V P		310
GCC GTC GGG TCG GTG CCC TTG CCC GTG CCG GTG CCG GTG CCA GTG CCC GTG CCG GTG CCT		930

FIG 1A

V P E P G L A P Q G P P G R T D G R A D 330
 GTG CCC GAG CCC GGC CTA GCT CCC CAG GGG CCC CCC GGC CGG ACC GAC GGC CGC GCG GAC 990
 K S K G Q V V L A T A I E I C V * 347
 AAG AGC AAA GGG CAG GTG GTG CTG GCC ACG GCC ATC GAG ATC TGC GTC TGA 1041
 ←SEQ ID NO:3↑
 GTCGCCTCCGCCGCCCTCGGACCCGGGAGCAGCCCGGGCCCCGCCCGAGCCGGTGCCCGGTGCGGCGGTAGGGAATGGA
 GCCACCTCGCCGCGGGGCAGGGGGCGCAGCGGTAGACTAGGCAGGACGCGGCCCGGCACCTGGTCCGTCCCCGGCGGGC
 TGGTGAGGGGGCCACCAAAGACCCCTACGCGGCCTGGTGAGCGGGGGCTTGGCCCAGAGGAGCCAAGCCGCACAGACC
 CGAGAATTCGGAGGCCACCACACAACACACACACACACATACACACACACACACACAGCCAGGAGCAAGGGAGC
 TTTCCGGGCCACACTCCCAGACGCCTCCCTGAGCCCTGGAACCCGGACTCGTTGCTCCTGGCCTTCCATACCCCTGGCA
 GATCATCCTGCGGTCCCACCCAGATCCCTCCTCCTCGCCATCCCATTCTGCCCCCTCCCCACCCTGGGTACAGAAAG
 GGACTGAAGTGTGGGCAGAGAGGGGGCTTAAGGCCCTGGGCACAGGCTGGGATCAGGGCAGTGAGCGAAGGGCAGCT
 GTGTCTGCCCTTCCTTCTGGAGGCTGGAGGGGAGAGGCCAAGCCCTTGAAAAATGTAGCAAATGTCTGGRWKGTGCGA
 TAAGTGCGTGTATGTGCGGGACAGGCCCGAGAAGCTAGTGACTCCTGCACACCCCCATTGCACAAATGAAATCACAGC
 CCAGGAGGGAGGGTAGCTTGGCACTGGCTGAGAAATAGAGCTCTCTCCCCGCCCTCCCCCTAACCACAAGGGATTGTC
 CTGACAACCTTGTGGGGATAGAAGGGCTCACAGGGCAGGGGTCTCAGCTGCCCCCATCCTTAGGGCAGGGGAGTTAGTGT
 GGAGCCGAGAGCAGGTCCCAGCTCCCCCTGCCAGCCGCACTGTCCAGGCCAGGGACCTCTGCCGGGTCTCCACGCC
 CTTGCCACACAGCCTAGACGTAGTAGCCTGGGCTTCCAGCAGGTGGCGAGCTGGTTCTGTGCTGGAAATTTCTCCTGGGT
 TTCTTGGGGTCAAACATGCCAACCTCCAAGACCCCATCCTCACGTCTCCCACTTTTCTGGCGCTGGAGTGTGCAGGGCG
 TAGGACCTGCATGTGTGGGTGTGAGAATGGGGGCCGGTGACACCAGGGGGCGAGTGTGTGACTAGGTGTGTGTGCACA
 TGTGTAGGGTGCAGACGCATGGGTGCCATCCTTTGCNTTCAATGACTGTGCGTCCAGACCCCAAAAAGCGGCCCCCCC
 ACCACACCCTGNTCCTCCCAGGCAGCTGTCCCAGGGCGCCCAGGCCTGCCTTGCAACCACAGCCCTCAGGAAATCCGGCA
 AGGAGGCCCCCTGCAGGTGGTTTCANGCCAGGTAGCAAAACAGAGACAACAGCAGCCCCGCCTGACCCCTGCCCTNT
 CTGTGGAGGCCCCGGGACCCCGCAATAAGCACCATGGGTGAGGCTGTCCCTGTCAGGGNCCCCTGCCAGGGTCCCTC
 CTGGGGTTCTGGGCCATTTGAGGGGCTCTTTGATGGGCCAGGCCNGCCAGAGTGAACCTCCGAGCACTTTCTGGCTGGT

FIG 1B

09916790 072701

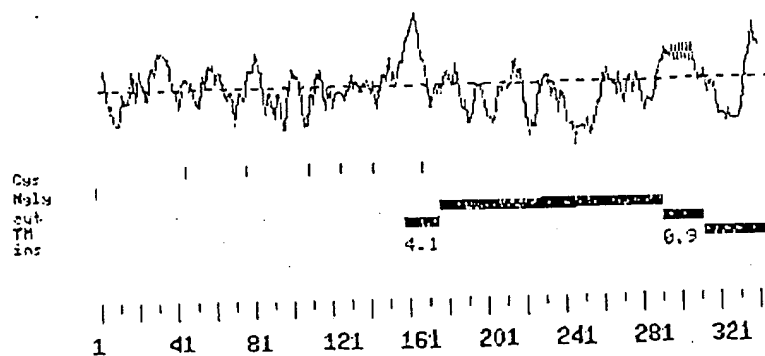


Fig. 2

*->vAvKilkkesls...lrEiqilkrIs.HpNIvrllgvfedtdhhly SEQ ID NO:7
 +A+K ++k++++ ++ lrE++i ++ls+ p+l++++v+ +t+d +
 32374 1 MALKFVNKSKTKlknfLREVSITNSLSsSPFIKVFDDVVFETEDCYV 47
 lvmEymegGdLfdylrrngplsekeakkialQilrGleYLHsngivHRDL
 + +Ey++ GdLfd++ + l+e+ +k+++ Q+ +l+++H++ vHRD+
 32374 48 FAQYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFMHRQLVHRDI 97
 KpeNIllden..gtvKiaDFGLArll.eklttfvGTpwYmmAPEvileg.
 KpeN+Ll +++ vK+aDFG+ r +++ + + GT++Y APEv + +
 32374 98 KPEVLLFDRecRRVKLADFGMTRRVgCRVKRVSGTIPYT-APEV-CQAg 145
rgysskvDvWSlGviLyElltggplfpgadlpaftggdevdqliif
 + ++ ++ vDvW++Gv+++ +ltg
 32374 146 radgLAVDTGVDVWAFGVLFVCVLTG----- 171
 vlklPfsdelpktridpleelfrikkr.....rlplpsncSeelkdL
 P++ + ++ ++ f+ r ++++ ++++ ++++ e+++
 32374 172 --NFPWEAA-----SGADAFEEFVRwqrgrlpgLPSQWRRFTEPALRM 213
 lkkcLnkDPskRpGsatakei<-*
 ++L++ P++R ake+
 32374 214 FQRLLALEPERRG---PAKEV 231

Fig. 3

Query: 226 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRPPAAGPLRLEAPGPKRTVLTESGSGS 285
 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDR P GPLRLEAPGPKRTVLTESGSGS
 Sbjct: 1 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRLP--GPLRLEAPGPKRTVLTESGSGS 58 SEQ ID NO:8
 Query: 286 R 286
 R
 Sbjct: 59 R 59

Fig. 4

Query: 321 PPGRTDGRADKSKGQVVLATAIEICV 346
 PPGRTDGRADKSKGQVVLATAIEICV
 Sbjct: 89 PPGRTDGRADKSKGQVVLATAIEICV 114 SEQ ID NO:9

Fig 5

Query: 166 FCVLTGNFPWEAASGADAFEEFVRWQGRPLPGLPSQWRRFTEPALRMFQRLLALEPERR 225
 +C + G FPW+ AS + E+ +W + + P LP ++ F+E AL++F++ L + R
 Sbjct: 3 YC-MKGKFPWQKASIMCKPYWEWEQWLKRKNPALPKKFNPFSEKALKLFKKSILTFRFKDR 61 SEQ ID NO:10
 Query: 226 GPAKEVFRFL-KHELTSELRR 245
 AK++ + L K +L ++R
 Sbjct: 62 WTAKDMRKCLAKEKLLKSVKR 82

Fig. 6

FO2220"0629T660

Query: 4 K F V N K S K T K L K N F L R E V S I T N S L S S S P F I I K V F D V V F E T E D C Y V F A Q E Y A P A G D L F D I I P 63
 K V SK + + L E + + L ++ F + I + + + Y + + Y + + + I
 Sbjct: 16 K M V A F S K R E E E R I L L E I D L Y K K L E N N E F V I D L M A H I V D D I T H Y L L F D K Y S Q -- N F L E Y I E 73 SEQ ID NO:11

Query: 64 P - Q V G L P E D T V K R C V Q Q L G L -- A L D F M H G R Q L V H R D I K P E N V L L F D R E C R R V K L A D F G 118
 ++G D + K G + A ++ + H G + H D I K P N + L + + K + D F G
 Sbjct: 74 E L K I G E V D E L K H L K Y F S G I V S A I E Q L H G F E F A H L D I K P A N I L -- K S G D T I K M I D F G 128

Fig. 7

Query: 47 V F A Q E Y A P A G D L F D I I P P Q V G L P E D T V K R C V Q ----- Q L G L A L D F M H ----- G R Q 91
 + A E + P G L D + V + D + + + Q Q + A L ++ H G ++
 Sbjct: 175 M I A L E W L P G G T L A D Y F Q F K V R E K D D S E R S P I Q L K D M L S I L Y Q V S Q A L K Y I H S Q L D E F G Q E 234 SEQ ID NO:12

Query: 92 L V H R D I K P E N V L L F D R E C R R -- V K L A D F G M T R R V G C R V K R V S G T I P Y T A P E V - C Q A G R A D 148
 L H I N V L + + + R + V K L D F G + G + I Y P E + C A R
 Sbjct: 235 L T H G R I F T R N V L V T E P D L R K C E V K L G D F G - D A P M G L E Y S -- T P I I A Y M P P E I L C C A E R I P 291

Query: 149 G L A V D T G V D V W A F G V L I F - C V L T G N F P 174
 + D V W F G V I + C + G P
 Sbjct: 292 P H R P E N -- D V W M F G V F I W E C L T L G A Q P 316

Fig. 8

Query: 77 V Q Q L G L A L D F M H G R Q L V H R D I K P E N V L L --- F D R E C R R V K L A D F G M T R --- R V G C R V K 128
 + Q L A ++ H ++ R D + K + N + L L F D E ++ + A D F G + V
 Sbjct: 319 I A Q L L E A C T Y L H K H K V A Q R D M K S D N I L L E Y D F D E I P Q L V V A D F G C A L A C D N W Q V D Y E S D 378 SEQ ID NO:13

Query: 129 R V S -- G T I P Y T A P E V C Q A G R A D G L A V D T G V - D V W A F G V L I F C V L T G N F P W E A A S G A D A F F 185
 V S G A P E + A + V + + D W A G L + V L T + P +
 Sbjct: 379 E V S L G G N A K T K A P E I A T A V P G K N V K V N F E M A D T W A A G G L S Y E V L T R S N P F Y K L L ----- 432

Query: 186 E E F V R W Q R G R L P G L P S Q 202
 + + Q L P L P S +
 Sbjct: 433 - D T A T Y Q E S E L P A L P S R 448

Fig. 9

Query: 68 L P E D T V K R C V Q Q L G L A L D F M H G R Q L V H R D I K P E N V L L F D R -- E C R R V K L A D F G M T R R V G C 125
 L P D ++ L A + D F + G + H R D I K P + N + + R R + L D F + G
 Sbjct: 647 L P V D Q L E A Y G D Y L F G A V D F L E G E G I W H R D I K P D N I A V R I R P N R T R E L V L I D F S L A -- G Y 703 SEQ ID NO:14

Query: 126 R V K R V - S G T I P Y T A P E V C Q A G R A D G L A V D T G V D V W A F G V L I F C V L T G N F P - W E A A S G A D A 183
 K + G T Y P V R + D + + A V + + + G P W S
 Sbjct: 704 P A K N T D A G T D G Y L D P F V D V I T R G --- S Y D S H A E R Y A V A V T L H Q M A S G E L P K W G D G S V L P R 760

Query: 184 F F E E F V R W Q R G R L P G L P S Q W R R F T E P A L R --- M F Q R L L A L E P E R R G P A K E V F R -- F L K 236
 + W P + ++ F + P A + R F Q + L + + R P + R + K
 Sbjct: 761 M T D P - K E W P --- Y P T I A A E -- A F - D P A V R D G L V A F F Q K A L H R D A G K R F P E L K P M R D A W R K 813

Query: 237 H E L T S E L R R R P S H R A R K P - P G D - R P P A A G 263
 L + S H R R P D P A G
 Sbjct: 814 V F L D A S Q T V P S S H R T R P A A P A D G A A P A E G 842

Fig. 10

09916790.072701

Query: 30 PFIIKVFDDVFETEDCYVFAQEYAPAGDLFDIIPPQVGLP----EDTVKRCVQQLGLALD 85
P I+ + +V E + C++ QE G + + G+P E+ + +QQL LD
Sbjct: 71 PGILAIENVSEEDRCFLVTQEND--GPILSLTQYLKGIPRKLTEEEIVDIIQQLCSLLD 128 SEQ ID NO:15

Query: 86 FMHGRQLVHRDIKPENVLL-FDRECRRVKLADFGMTRRVGCR-----VKRV 130
++H L H +V + F + L D G + R +++++
Sbjct: 129 YVHSEGLAHGQWNLHSHVHIHFLNGVPNIYLPDLGFASLIRERMFQDGFMDQDEENRESIEKI 188

Query: 131 SGTIPYTAPEVCQAGRADGLAVDTGVDVWAFGVLIFCVLTGNFPWEAASGADAFEEFV 189
+ + PE Q +G DT +AFG + + +L G FPW F +F+
Sbjct: 189 RDRLLFHTPEGKQT---NGRETD---YAFGAITYYLLFGFFPWGIFPKPSKCFPDI 240

Fig. 11

Query: 29 SPFIKVFDDVFETEDC-YVFAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFM 87
SP ++ V D++ E E VF E L +++ PE ++ L L
Sbjct: 82 SPHVLPRDLIDEGEWLSLVF--EPRRTITLRELLSAGPVSPE-LLQPLTTALFEGLSAA 138 SEQ ID NO:16

Query: 88 HGRQLVHRDIKPENVLLFDRECRRVKLADFGMTRRVGCRVKRVSGTIP-YTAPEVCQAGR 146
H L+H I PE V FD + +R LA+FG+ RR ++ P Y APE+ G
Sbjct: 139 HQGALLHTQISPEAVW-FDTQ-KRPLLAEFGLARRTAQELRDHWPHDPRYAAPELLSGG- 195

Query: 147 ADGLAVDTGVDVWAFGVLIFCVLTGNFPWEAASGADAFEEFVVRWQGRRLP----GLPSQ 202
D++A + EAA+G A R Q RLP G+P Q
Sbjct: 196 ----PYTPQTDLYALAATLL-----EAATGT-ALSPVSARQQGVRLPSWPAGIPPQ 241

Query: 203 WRRFTEPALRMFORLLALEPERRGPAKEVFRFLKH-ELTSELRRRPSHRARKPPGDRPPA 261
E L++ + A+ A EV L+ + T + + A P PPA
Sbjct: 242 VAHALESCLQDPAVRAVS-----AAEVLEELRRAQPTQAILSQQEPPAPPPSVPSPPA 295

Query: 262 A 262
A
Sbjct: 296 A 296

Fig. 12

102220"0629T660

09916790.072701

CTTCCTCTTCCTGTGCTCAGTCCCATTAACTGCCATACCACGGCTCCTCGTCTTCCCAATCCCTCACCCAGTATTTT SEQID NO:4
 CAATCGACCCCCCGTCCCCCGCACCTCTTTCTCTCTCGCTATATGTCCTTTTCGTGGCCAGTTTGGGCAAGGGGAA
 GGACACCACAAGTCGGGGTCTTTCTCAGCGTTGGGTGCGGGTGGCTGTGAGGGCGGAAGAAAAGGCCAGGCTGAGGGG
 AGGGTAGAGGGTGAAAAGCTCGGATCTGTGTTGGGGAAAGGCCAGGCTTGCGCTCCTCGCCGGGTCCGCGAAGGTTAA
 CCTTGGCTGACTTGGCTCGCGAGCAAAGGGCAGCGTCTGAGCTCCCGCGTTCAGGAGTGGCCTCTTTTGTAGGAGCA
 CCTGAAATGCAGCGTCTGGTGCCTAAGCCGTAGCGGCAGCAGCAGCCACAGCGACAGCGCTGGGGCCCTGTGTAGAAG

CTCCATCCCCCTTGCTTTGTGCTTGCTGCGTCCCCAGACTCAGAGATTATCTTAGAAGACCTAGGACTCCAAAA

M	F	P	L	K	D	A	E	M	G	A	F	T	F	F	A	S	A	L	P	20	SEQ ID NO:5
ATG	TTT	CCC	CTG	AAG	GAC	GCT	GAA	ATG	GGA	GCC	TTT	ACC	TTC	TTT	GCC	TCG	GCT	CTG	CCA	60	
↑SEQ ID NO:6→																					
H	D	V	C	G	S	N	G	L	P	L	T	P	N	S	I	K	I	L	G	40	
CAT	GAT	GTT	TGT	GGA	AGC	AAT	GGA	CTT	CCT	CTC	ACA	CCA	AAT	TCC	ATC	AAA	ATT	TTA	GGG	120	
R	F	Q	I	L	K	T	I	T	H	P	R	L	C	Q	Y	V	D	I	S	60	
CGC	TTT	CAA	ATC	CTT	AAA	ACC	ATC	ACC	CAT	CCC	AGA	CTC	TGC	CAG	TAT	GTG	GAT	ATT	TCT	180	
R	G	K	H	E	R	L	V	V	V	A	E	H	C	E	R	S	L	E	D	80	
AGG	GGA	AAG	CAT	GAA	CGA	CTA	GTG	GTC	GTG	GCT	GAA	CAT	TGT	GAA	CGT	AGT	CTG	GAA	GAC	240	
L	L	R	E	R	K	P	V	S	C	S	T	V	L	C	I	A	F	E	V	100	
TTG	CTT	CGA	GAA	AGG	AAA	CCT	GTG	AGC	TGT	TCA	ACG	GTT	TTG	TGT	ATA	GCA	TTT	GAG	GTT	300	
L	Q	G	L	Q	Y	M	N	K	H	G	I	V	H	R	A	L	S	P	H	120	
CTT	CAG	GGC	TTG	CAG	TAT	ATG	AAC	AAA	CAT	GGT	ATA	GTA	CAC	AGG	GCA	TTG	TCT	CCT	CAT	360	
N	I	L	L	D	R	K	G	H	I	K	L	A	K	F	G	L	Y	H	M	140	
AAT	ATC	CTG	TTG	GAC	CGA	AAG	GGA	CAT	ATT	AAA	TTG	GCT	AAA	TTT	GGA	CTT	TAT	CAC	ATG	420	
T	A	H	G	D	D	V	D	F	P	I	G	Y	P	S	Y	L	A	P	E	160	
ACA	GCT	CAT	GGT	GAT	GAT	GTT	GAT	TTC	CCA	ATA	GGG	TAT	CCC	TCG	TAC	TTG	GCC	CCT	GAG	480	
V	I	A	Q	G	I	F	K	T	T	D	H	M	P	S	K	K	P	L	P	180	
GTA	ATT	GCA	CAG	GGA	ATT	TTC	AAA	ACC	ACT	GAT	CAC	ATG	CCA	AGT	AAA	AAA	CCA	TTG	CCT	540	
S	G	P	K	S	D	V	W	S	L	G	I	I	L	F	E	L	C	V	G	200	
TCT	GGC	CCC	AAA	TCA	GAT	GTA	TGG	TCT	CTT	GGA	ATC	ATT	TTA	TTT	GAG	CTT	TGT	GTG	GGA	600	
R	K	L	F	Q	S	L	D	I	S	E	R	L	K	F	L	L	T	L	D	220	
AGA	AAA	TTA	TTT	CAG	AGC	TTG	GAT	ATT	TCT	GAA	AGA	CTA	AAA	TTT	TTG	CTT	ACT	TTG	GAT	660	
C	V	D	D	T	L	I	V	L	A	E	E	H	G	C	L	D	I	I	K	240	
TGT	GTA	GAT	GAC	ACT	TTA	ATA	GTT	CTG	GCT	GAA	GAG	CAT	GGT	TGT	TTG	GAC	ATT	ATA	AAG	720	
E	L	P	E	T	V	I	D	L	L	N	K	C	L	T	F	H	P	S	K	260	
GAG	CTT	CCT	GAA	ACT	GTG	ATA	GAT	CTT	TTG	AAT	AAG	TGC	CTT	ACC	TTC	CAT	CCT	TCT	AAG	780	

Fig. 13A

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R	P	T	P	D	E	L	M	K	D	K	V	F	S	E	V	S	P	L	Y	280
AGG	CCA	ACC	CCA	GAT	GAA	TTA	ATG	AAG	GAC	AAA	GTA	TTC	AGT	GAG	GTA	TCA	CCT	TTA	TAT	840
T	P	F	T	K	P	A	S	L	F	S	S	S	L	R	C	A	D	L	T	300
ACC	CCC	TTT	ACC	AAA	CCT	GCC	AGT	CTG	TTT	TCA	TCT	TCT	CTG	AGA	TGT	GCT	GAT	TTA	ACT	900
L	P	E	D	I	S	Q	L	C	K	D	I	N	N	D	Y	L	A	E	R	320
CTG	CCT	GAG	GAT	ATC	AGT	CAG	TTG	TGT	AAA	GAT	ATA	AAT	AAT	GAT	TAC	CTG	GCA	GAA	AGA	960
S	I	E	E	V	Y	Y	L	W	C	L	A	G	G	D	L	E	K	E	L	340
TCT	ATT	GAA	GAA	GTG	TAT	TAC	CTT	TGG	TGT	TTG	GCT	GGA	GGT	GAC	TTG	GAG	AAA	GAG	CTT	1020
V	N	K	E	I	I	R	S	K	P	P	I	C	T	L	P	N	F	L	F	360
GTC	AAC	AAG	GAA	ATC	ATT	CGA	TCC	AAA	CCA	CCT	ATC	TGC	ACA	CTC	CCC	AAT	TTT	CTC	TTT	1080
E	D	G	E	S	F	G	Q	G	R	D	R	S	S	L	L	D	D	T	T	380
GAG	GAT	GGT	GAA	AGC	TTT	GGA	CAA	GGT	CGA	GAT	AGA	AGC	TCG	CTT	TTA	GAT	GAT	ACC	ACT	1140
V	T	L	S	L	C	Q	L	R	N	R	L	K	D	V	G	G	E	A	F	400
GTG	ACA	TTG	TCG	TTA	TGC	CAG	CTA	AGA	AAT	AGA	TTG	AAA	GAT	GTT	GGT	GGA	GAA	GCA	TTT	1200
Y	P	L	L	E	D	D	Q	S	N	L	P	H	S	N	S	N	N	E	L	420
TAC	CCA	TTA	CTT	GAA	GAT	GAC	CAG	TCT	AAT	TTA	CCT	CAT	TCA	AAC	AGC	AAT	AAT	GAG	TTG	1260
S	A	A	A	T	L	P	L	I	I	R	E	K	D	T	E	Y	Q	L	N	440
TCT	GCA	GCT	GCC	ACG	CTC	CCT	TTA	ATC	ATC	AGA	GAG	AAG	GAT	ACA	GAG	TAC	CAA	CTA	AAT	1320
R	I	I	L	F	D	R	L	L	K	A	Y	P	Y	K	K	N	Q	I	W	460
AGA	ATT	ATT	CTC	TTC	GAC	AGG	CTG	CTA	AAG	GCT	TAT	CCA	TAT	AAA	AAA	AAC	CAA	ATC	TGG	1380
K	E	A	R	V	D	I	P	P	L	M	R	G	L	T	W	A	A	L	L	480
AAA	GAA	GCA	AGA	GTT	GAC	ATT	CCT	CCT	CTT	ATG	AGA	GGT	TTA	ACC	TGG	GCT	GCT	CTT	CTG	1440
G	V	E	G	A	I	H	A	K	Y	D	A	I	D	K	D	T	P	I	P	500
GGA	GTT	GAG	GGA	GCT	ATT	CAT	GCC	AAG	TAC	GAT	GCA	ATT	GAT	AAA	GAC	ACT	CCA	ATT	CCT	1500
T	D	R	Q	I	E	V	D	I	P	R	C	H	Q	Y	D	E	L	L	S	520
ACA	GAT	AGA	CAA	ATT	GAA	GTG	GAT	ATT	CCT	CGC	TGT	CAT	CAG	TAC	GAT	GAA	CTG	TTA	TCA	1560
S	P	E	G	H	A	K	F	R	R	V	L	K	A	W	V	V	S	H	P	540
TCA	CCA	GAA	GGT	CAT	GCA	AAA	TTT	AGG	CGT	GTA	TTA	AAA	GCC	TGG	GTA	GTG	TCT	CAT	CCT	1620
D	L	V	Y	W	Q	G	L	D	S	L	C	A	P	F	L	Y	L	N	F	560
GAT	CTT	GTG	TAT	TGG	CAA	GGT	CTT	GAC	TCA	CTT	TGT	GCT	CCA	TTC	CTA	TAT	CTA	AAC	TTC	1680
N	N	E	A	L	A	Y	A	C	M	S	A	F	I	P	K	Y	L	Y	N	580
AAT	AAT	GAA	GCC	TTG	GCT	TAT	GCA	TGT	ATG	TCT	GCT	TTT	ATT	CCC	AAA	TAC	CTG	TAT	AAC	1740
F	F	L	K	D	N	S	H	V	I	Q	E	Y	L	T	V	F	S	Q	M	600
TTC	TTC	TTA	AAA	GAC	AAC	TCA	CAT	GTA	ATA	CAA	GAG	TAT	CTG	ACT	GTC	TTC	TCT	CAG	ATG	1800
I	A	F	H	D	P	F	L	S	N	H	L	N	E	I	G	F	-	P	D	620
ATT	GCA	TTT	CAT	GAT	CCA	GAG	CTG	AGT	AAT	CAT	CTC	AAT	GAG	ATT	GGT	TTC	ATT	CCA	GAT	1860
L	Y	A	I	P	W	F	L	T	M	F	T	H	V	F	P	L	H	K	I	640
CTC	TAT	GCC	ATC	CCT	TGG	TTT	CTT	ACC	ATG	TTT	ACT	CAT	GTA	TTT	CCA	CTA	CAC	AAA	ATT	1920

Fig. 13B

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F H L W D T L L L G N S S F P F C I G V	660
TTC CAC CTC TGG GAT ACC TTA CTA CTT GGG AAT TCC TCT TTC CCA TTC TGT ATT GGA GTA	1980
A I L Q Q L R D R L L A N G F N E C I L	680
GCA ATT CTT CAG CAG CTG CGG GAC CGG CTT TTG GCT AAT GGC TTT AAT GAG TGT ATT CTT	2040
L F S D L P E I D I E R C V R E S I N L	700
CTC TTC TCC GAT TTA CCA GAA ATT GAC ATT GAA CGC TGT GTG AGA GAA TCT ATC AAC CTG	2100
F C W T P K S A T Y R Q H A Q P P K P S	720
TTT TGT TGG ACT CCT AAA AGT GCT ACT TAC AGA CAG CAT GCT CAA CCT CCA AAG CCA TCT	2160
S D S S G G R S S A P Y F S A E C P D P	740
TCT GAC AGC AGT GGA GGC AGA AGT TCG GCA CCT TAT TTC TCT GCT GAG TGT CCA GAT CCT	2220
P K T D L S R E S I P L N D L K S E V S	760
CCA AAG ACA GAT CTG TCA AGA GAA TCC ATC CCA TTA AAT GAC CTG AAG TCA GAA GTA TCA	2280
P R I S A E D L I D L C E L T V T G H F	780
CCA CGG ATT TCA GCA GAG GAC CTG ATT GAC TTG TGT GAG CTC ACA GTG ACA GGC CAC TTC	2340
K T P S K K T K S S K P K L L V V D I R	800
AAA ACA CCC AGC AAG AAA ACA AAG TCC AGT AAA CCA AAG CTC CTG GTG GTT GAC ATC CGG	2400
N S E D F I R G H I S G S I N I P F J A	820
AAT AGT GAA GAC TTT ATT CGT GGT CAC ATT TCA GGA AGC ATC AAC ATT CCA TTC AGT GCT	2460
A F T A E G E L T Q G P Y T A M L Q N F	840
GCC TTC ACT GCA GAA GGG GAG CTT ACC CAG GGC CCT TAC ACT GCT ATG CTC CAG AAC TTC	2520
K G K V I V I V G H V A K H T A E F A A	860
AAA GGG AAG GTC ATT GTC ATC GTG GGG CAT GTG GCA AAA CAC ACA GCT GAG TTT GCA GCT	2580
H L V K M K Y P R I C I L D G G I N K I	880
CAC CTT GTG AAG ATG AAA TAT CCA AGA ATC TGT ATT CTA GAT GGT GGC ATT AAT AAA ATA	2640
K P T G L L T I P S P Q I *	894
AAG CCA ACA GGC CTC CTC ACC ATC CCA TCT CCT CAA ATA TGA	2682

←SEQ ID NO:6↑

AGAACCAAGAGTGTGACTGCCAAACTTAGTGTGGCATCAGCACCAACAGCACAGTTCTTCATATCCACGCCACTCTCA
 GACAAACTAGATGTCCAGATTGTTGCATTTCCGTAAAGTTTGTACAGAGACATTTTTTAAATCTCATAACCCACATG
 TTCAGTTATCCATGCAAGAACTTGACTCTACATGTATTGCTGAAAGAATTTTCTTAACAGTGAAATCTGATCATATAT
 TTTTACCACACTGCCACATAAAGCCCAAGAAATTCAGCTGACAAGACAGATTTAGCATTATCAAGAAATC ATTTGCC
 CTGAAAAAGCTGTCCTCCATTGTACTGAACAGACAGTCCTGTGATTGTGTTATTTAGAAACATACACTGAATGTGGGC
 TGAAATCATCATCTTTCCATAATGAAAAGTGAAGAACTATTCACAATGCATTTCCTTATAAAATAAATGCTACATTTAGTA
 ACTCATTTACCCAAACAAGAAAGATGTGTGTGTGTGTGTATAGGAAGTGGAGTTTATCCCCATTGCA AAACT
 AATACTTACTCCCAGAAAAATGAAATTTAGAAACCATTATATTTGATAGAATATTTGGTCAGTTCCTGTAGCAAAGAC
 GAATGGCTTAAACAAATTTTCTAGTTTCTTTATCACATGAAAGTCTGTACAGTCAGTCCAGGGCTAGTCTACTGGTTTC

Fig. 13C

CTGATCATTAAGAACTCATTACCTTCTCTCATTGCTTTACAAACCTCAATATGTGGCATCCATCTCATGGATGAAAATG
GCTCCTCAGCTTCTACCATCACATCTGCTATCTAGAAGGAAGAGAATGAGGGAAGGAGGGAGGGGATGAAGAGAAAAGA
AGGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FO220"0629T660

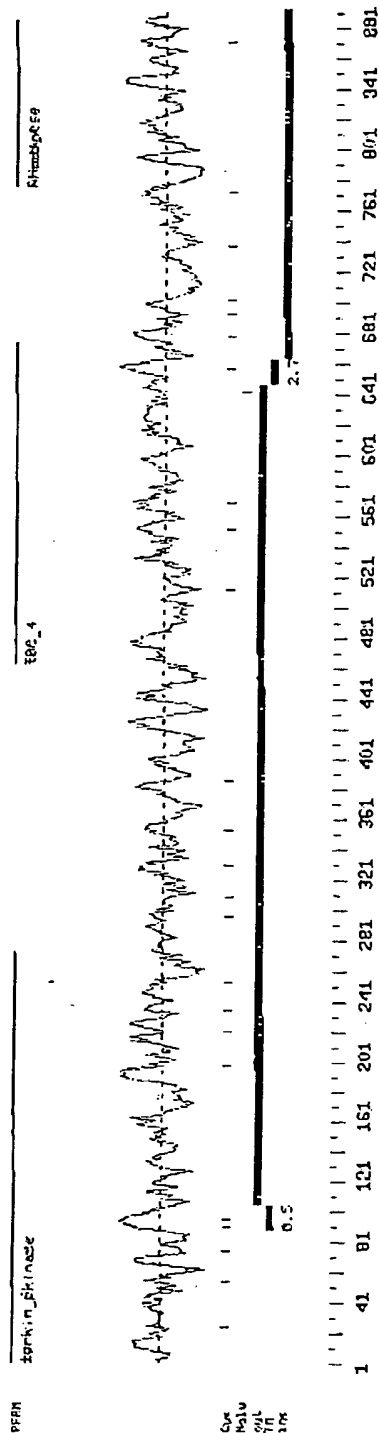


Fig. 14

```

*->qilkrlsHpNIvrllgvfedtdhlylvmEymegGdLfdylrrngpl SEQ ID NO:17
qilk++ Hp ++++ ++ + ++l +v E++e +L d+lr+++p
18431 43 QILKTITHPRLCQYVDISRGKHERLVVVAEH CER-SLEDLLRERKPV 88

sekeakkialQilrGleYlHsngivHRDLKpenILldengtVkiADFGLA
s +++ia ++l+Gl+Y+ +givHR L p NILld++g++K+a FGL
18431 89 SCSTVLICIAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLAKEFGLY 138

rll...eklttfVGTpwYmmAPEvi.....leg.rgysskvDv
++ G p Y APEvi ++ +++++ + + + + ++k+Dv
18431 139 HMTahgDDVDFPIGYPSYL-APEVIAqgiktt dhmpSKKpLPSGPKSDV 187

WSlGviLyElltggplfp gadlpftggdevdqliifvklPfsdelpkt
WSlG+iL+El+ g++lf+++d ++ l +
18431 188 WSLGIILFELCVGRKLFQSLD-----ISERLKFLTL 219

ridpleelfrikkr.rlpplsncSeelkdLlkkcLnkDPskRpGsatake
++ ++ +++ l++ +++e+++dLl+kcL++ PskRp t e
18431 220 DCVDDTLIVLAEHGLDIIKELPETVIDLLNKCLTFHPSKRP---TPDE 266

ilnhpwf<-*
+++++ f
18431 267 LMKDKVF 273

```

Fig. 15

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*->vrqgvpsSlRgkVWklIlLgaqelnncIltdnfkgldlfglvpllla SEQ ID NO:18
r +p +Rg W++llg +
18431 463 ARVDIPPLMRGLTWAALLGVEGAI----- 486

dkdeYeellnknkektvqdqneKssvgirrl dyVEAVEKHPLSDDNDKTK
Y++++ ++ +t
18431 487 -HAKYDAIDKDTPIPT----- 501

GSLekgsdekalklredldkIekDlsRTfpdeiffqtrlaeqqlkdkdql
+ +Ie D+ R+ + +++
18431 502 -----DRQIEVDIPRCHQYDELL----- 519

daydkDEfddeddkneppsikQLrrlLvaYswknpqehlgYvQGMnvils
+p+++++ rr+L a ++ +p+ l Y QG + +
18431 520 -----SSPEGHAKFRRVLKAWVVSHPD--LVYWQGLDSLCA 553

pLLlf.lkhgvdIdeideeqAFwclvkLmdnylpqkyflndls.glnedl
p+L++++ +e A++c ++++ +yl + +fl+d s+ +e l
18431 554 PFLYLnFN-----NEALAYACMSAFIPKYLYN-FFLKDNShVIQEYL 594

rvLdslvkeslPeLyshlkkkenktgsgkKknllaldltllifafpwlLt
v++ + + +PeL++hl+ + +++++a+pwlLt
18431 595 TVFSQMIAFHDPELS NHLNEI-----GFIPDLYAIPWFLT 629

lFarelPleivlrIwDilftyYlgshflifvalAiLkllksklkh<-*
F+ ++Pl +++++WD l++ +s+f++ +++AiL++l++ ll+
18431 630 MFTHVFPLHKIFHLWDTLLLG--NSSFPFCIGVAILQQLRDRLLAN 673

```

Fig. 16

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Query: 459 IWKEARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDT-----PIPTDRQIEVDIPRC 512
 I +E +D+PP +RG W LL V + +Y +D P P DRQ+EVDIPRC
 Sbjct: 1 IQRETNIDVPPTLRGEVWGCLLRVPPSARTRYALLDHAVHHTAAKPTPHDRQLEVDIPRC 60 SEQ ID NO:19

Query: 513 HQYDELLSSPEGHAKFRRVLKAWVSH--PDLVYWQGLDLSLCAPFLYLNFNNEALAYACM 570
 HQY LL+SP G A+ RR+LKAW + + P+ VYWQGLDLSLCAPFL +N +EALA+A +
 Sbjct: 61 HQYHPLLNSPSGSAQLRRILKAWQIVYLRPEHVYWQGLDLSLCAPFLTVNNRDEALAFACL 120

Query: 571 SAFIPKYLYNFFLKDNSHVIQEYLTVFSQMIAFHDPESNHLNEIGFIPD 620
 +AF+ +Y++ F+LKDNS VI+EYL F + A+HDP L HL GF P+
 Sbjct: 121 NAFVNRYYHWFYKDNSEVIKEYLGKFYHLTAYHDPLLYQHLKINGFDPE 170

Fig. 17

Query: 27 NGLPLTPNSIKILGRFQILKTITHPRLCQYVDISRGKHER--LVVVAEHCERSLEDLLRE 84
 NGLPLTP + ++LGRF L+ + H LCQY+ RGKHER +VV EH +LED +
 Sbjct: 1 NGLPLTPPAKQMLGRFPYLQELQHDHLCQYLFIRGKHERDLTIVVMEHYGMNLEDYAKR 60 SEQ ID NO:20

Query: 85 RKPVSCSTVLCIAFEVLQGLQYMNKHGIVHRALSPHNILL---DRKGHIKLAKFGLYHM 140
 P + +++ G+ Y+++H IVH L P++I + +RK +KL +GL+HM
 Sbjct: 61 HPPKDEAQNNNFYQIACGINYLHRHHIVHHNLHPNHIYITDDGNRKL SVKLFNYGLHHM 120

Query: 141 TAHGDDVDFPIGYPSYLAPEVIAQGIKTTDHMXXXXXXXXXXXXXVWSLGIILFELCVG 200
 T +G FPIG Y+APE I D++ DVW LG I+ ++ +G
 Sbjct: 121 TNYGKYTPFPIGNGRYMAPE----RILNDNDNLFAATYQS----DVWELGFIMLQIYLG 171

Query: 201 RKL 203
 +L
 Sbjct: 172 IEL 174

Fig. 18

Query: 322 IEEVYYLWCLAGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRXXXXXXXXXXXXX 381
 + ++Y+LW LAGGD++ EL + +IRS+ PI LP + G S GR
 Sbjct: 100 LSQIYHLWQLAGGDVQAEKKEGLIRSEAPILGLPQIVRLSGASVCPGRSQAQLMDDRVV 159 SEQ ID NO:21

Query: 382 XXXXCQLRNLKDVGGGEAFYPLLEDDQSNLPHSNSNNELSAATLPLIIREKDTEYQLNR 441
 L RL + ++PLL + P ++ EL LPL+IREKD EYQ R
 Sbjct: 160 PLRLKALLQRLSGLPAAVYFPLLHSPR--FP-AHFARELQE--LPLVIREKDIEYQFQR 213

Query: 442 IILFDRLLKAYPYKKNQ 458
 + LF RLL+ YP+ Q
 Sbjct: 214 VRLFARLLQGYPHTAEQ 230

Fig. 19

Query: 207 LDISERLKFLLTLCVDDTLIVLAEHEGCLDIKELPETVIDLLNKCLTFHPSKRPTPDE 266
 L +S ++ +L + L +A EH C + ++ + + LL CL+ P +RP P E
 Sbjct: 4 LKLSNVVRKILAFGKSNGALEKIAREHQCHERYVQMDQRLRQLLESCLSVLPKRRPLPGE 63 SEQ ID NO:22

Query: 267 LMKDKVFSEV 276
 L++ +F EV
 Sbjct: 64 LLEHPIFEV 73

Fig. 20

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Query: 636 PLHKIFHLW 644
 PL +I+HLW
 Sbjct: 99 PLSQIYHLW 107 SEQ ID NO:23

Fig. 21

Query: 621 LYAIPWFLTMFTHVPLHKIFHLWDTLGNSFPFCIGVAILQQLRDRLL-ANGFNECI 679
 LYA WFLT+F PL + +WD S F + +A+L+ ++ LL A+ F E +
 Sbjct: 1 LYAFQWFLTLFARELPLETVLRIWDCFFYEGSKILFRVALALLKMHKEELLQADDFEEML 60 SEQ ID NO:24

Query: 680 -LLFSDLP-----EIDIERCVRESINL 700
 L + LP E D R + E+ N+
 Sbjct: 61 EFLQNMLPKRYRSEEDARLLLEEACNI 87

Fig. 22

Query: 72 EHCERSLEDLLRERKPVSCSTV---LCIAFEVLQGLQYM---NKHGIVHRALSPHNILL 124
 E E+ + + E+K S V + IA+++ +GL+Y+ NK I+HR L P NILL
 Sbjct: 136 EMMEKLQKQSMSEKKMEEMSWVSQLMKIAYQIAKGLEYLHKSNSKNQNIHRDLKPENILL 195 SEQ ID NO:25

Query: 125 DR---KGH-----IKLAKFGLYHM 140
 D KG +K+A FGL M
 Sbjct: 196 DNNMVAKGDSEIKVVKIADFGARM 220

Fig. 23

Query: 152 GYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXXDVWSLGIILFELCVGRKLF--QSLDI 209
 G PSY+ + + + + DVWS G+IL+EL G+ F S ++
 Sbjct: 245 GTPSYV--KYVGTRWYMAPEVLGSSYGQYSEKSDVWSFGVILYELLTGKPPFFPGSSEV 302 SEQ ID NO:26

Query: 210 SE-RLKFLTLDCVDDTLIVLAEHGCGLDIIKE---LP----ETVIDLLNKCLTFHPSKR 261
 ++ ++ ++ V + + + KE P E V DL+ KC P KR
 Sbjct: 303 NDSQMNEIMKETMVKSAEYEMPMKMPPESSKESMSCPSMSSEAVKDLIKCKWQKDPEKR 362

Query: 262 PTPDELMKDKVFSEV 276
 PT +++++ E+
 Sbjct: 363 PTFAQVVEELSAHEI 377

Fig. 24

Query: 740 PPKT-DLSRESIPLNDLKSEVSPRISAEDLIDLCELTVTGHFXXXXXXXXXXXXXXXXLLVVD 798
 PP+ D+ + L L+ E PRISA+D+ L + L ++D
 Sbjct: 29 PPQALDIGVADVELKHLQQEQCPRISAKDVQFLD-----NSPAELALID 73 SEQ ID NO:27

Query: 799 IRNSEDfirghisGSINIPFSAAFTAEGELTQGPYTAMLQNFKGKIVIVGVHAKHTAEF 858
 +R+ +F R H+ SINIPF+ E L + +GK++V V ++ +H+ E
 Sbjct: 74 LRSVVEFGRVHVPHSINIPFATVQLGEQRLEALQVPQLEAQLRGKIVVCVSNIHQHSVEV 133

Query: 859 AAHLVKMK 866
 L ++K
 Sbjct: 134 GHPLAQLK 141

Fig. 25

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Query: 693 CVRESINLFCWTPKSATYRQHA---QPPKXXXXXXXXXXAPYFSAECPDPKTDL---- 745
 CV ES ++ TPKS T+RQHA QPP+ +CP D+
 Sbjct: 3 CVLESQKMYEATPKSITHRQHALRLQPPQALDIGVADVELKHLQQEQCPRISAKDVQFLL 62 SEQ ID NO:28

Query: 746 --SRESIPLNDLKSEVS-PRISAEDLIDLCELTV 776
 S + L DL+S V R+ I++ TV
 Sbjct: 63 DNSPAELALIDLRSVVEFGRVHVPHSINIPFATV 96

Fig. 26

Query: 856 AEFAAHLVKMKYPRICILDGGIN---KIKPTGLLT 887
 ++F+ LV R CIL G N I+P L++
 Sbjct: 152 SQFSHFLVACGVQRTCILHKGFNVLSIEPNILIS 186 SEQ ID NO:29

Fig. 27

Query: 506 EVDIPRCHQYDELLSSPEGHAKFRRLKAWVVSHPD--LVYWQGLDSLCAFLYLNFNNE 563
 + DI C +Y+ P + + + L+ + V +P ++ + G APF YL
 Sbjct: 336 DTDIGGCCFEYNTF-PPPGKYRKGLEEYAVFYPPNGVIPFHGFCMYAAPFCYLYHEPS 394 SEQ ID NO:30

Query: 564 ALAYACMSAFIPKYLYNFFLKDNSHV--IQEYLTVFSQMIAFHDPELSNHLNEIGFIPDL 621
 L Y +I +Y + N+H I +F + + + ++P+L H EIG P
 Sbjct: 395 KLYYTFREFYI-RYCHRLHTI-NTHPQGIVSLCLLFEKLLQTYEPQLWYHFREIGAQLR 452

Query: 622 YAIPWFLTMFTHVFLHKIFHLWDTLLLGNS 652
 + W + F+ P ++ LWD +L NS
 Sbjct: 453 ISFKWMMRAFSGHLPPDQLLLWDRILGYNS 483

Fig. 28

Query: 77 SLEDLLRERKPVSCSTVLC--IAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLA 134
 S LLR P S L I F ++GL Y++++G +HR++ +IL+ G + L+
 Sbjct: 5 SASQLLRITYFPEGMSETLIRNIFGAVRGLNYLHQNGCIHRSIKASHILISGDGLVTLG 64 SEQ ID NO:31

Query: 135 FG-LYHMTAHGDD---VDFP---IGYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXD 186
 L+ + HG DFP +L+PE++ Q + H D
 Sbjct: 65 LSHLHSLVKHGQRHRAVYDFPQFSTSVQPWLSPELLRQDL-----H-----GYNVKS 112

Query: 187 VWSLGIILFELCVGRKLFQSLDISERL 213
 ++S+GI EL G+ FQ + ++ L
 Sbjct: 113 IYSVGITACELASGVFPQDMHRTQML 139

Fig. 29

Query: 240 KLPETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEV 276
 K L+ CL P KRP+ L+ F ++
 Sbjct: 198 KTFSPAFFSLVQLCLQQDPEKRPASASSLLSHVFFKQM 234 SEQ ID NO:32

Fig. 30

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Query: 596 VFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFLPHKIFHLWDTLLLGNSFP 655
 +F ++ +HDPEL NHL+ PD+Y + WF ++F LWD + F
 Sbjct: 18 LFRLLQYHDPELCNHLDTTKCTPDMYTLNWFGSLFASCCSTEVCHALWDLYIQQADPFM 77 SEQ ID NO:33

Query: 656 -FCIGVAILQQLRDRLL---ANGFNECILLFSDLP-EIDIE 691
 F + + IL ++ +L ++ E I ++P +++IE
 Sbjct: 78 VFFLALIILINAKEEILQMKSDSKEEVIKFLENMPCQLNIE 118

Fig. 31

Query: 796 VVDIRNSEDfirghisgsini 816
 +VD R +E + GH+S + ++
 Sbjct: 194. IVDCRPAEQYNAGHLSTAFHL 214 SEQ ID NO:34

Fig. 32

Query: 112 IVHRALSPHNILLDRKGHIKLAKFGLYHMTAHGDDVD--FPIGYP--SYLAPEVIAQGIF 167
 ++HR + P +IL+ ++G KLA F + +D + FP Y + P + +
 Sbjct: 1 VIHRNICPESILITKRGSWKLAGFDFCVSAQNPNQENYFPCHYEWDPRIPPLPLQPNLD 60 SEQ ID NO:35

Query: 168 KTTDHMXXXXXXXXXXXXDVWSLGIILFELCVGRKLFQSLDISERLKFLTLDCVDDTLI 227
 D++SLG +++ + G K +D + ++ + +TL
 Sbjct: 61 YLAPEYVTSSTCTVGSASDMFSLGCLIIYAIYNGGKPL--IDANNDEYKSNYKYMNTLN 118

Query: 228 VLAEHGCGLDIIKELPETVIDLLNKCLTFHPSKRPTPDELMKDKVF 273
 L H ++ + PE + + L + L+ P+ RPT EL K F
 Sbjct: 119 SLT--HESMNNLP--PENLKESLKRMLSMDPTVRPTAQELTLIKYF 160

Fig. 33

Query: 744 DLSRESIPLNDLKSEVSPRI--SAEDL-IDLCE 773
 DL + P D+KS + P + + ED I +C+
 Sbjct: 273 DLLLQKTPPEDIKSNILPMLYYAFEDSDIQC 305 SEQ ID NO:36

Fig. 34

09916790.072701